

SEQUENCE LISTING

## (1) GENERAL INFORMATION:

(i) APPLICANT: Bahija Jallal  
Gregory D. Plowman

(ii) TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF  
PTP04 RELATED DISORDERS

(iii) NUMBER OF SEQUENCES: 18

## (iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Lyon & Lyon  
(B) STREET: 633 West Fifth Street  
Suite 4700  
(C) CITY: Los Angeles  
(D) STATE: California  
(E) COUNTRY: U.S.A.  
(F) ZIP: 90071-2066

## (v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
storage  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: IBM P.C. DOS 5.0  
(D) SOFTWARE: FastSEQ for Windows 2.0

## (vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned  
(B) FILING DATE: Herewith  
(C) CLASSIFICATION:

## (vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 60/047,222  
(B) FILING DATE: May 20, 1997

## (viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Warburg, Richard J.  
 (B) REGISTRATION NUMBER: 32,327  
 (C) REFERENCE/DOCKET NUMBER: 234/253

## (ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (213) 489-1600  
 (B) TELEFAX: (213) 955-0440  
 (C) TELEX: 67-3510

## (2) INFORMATION FOR SEQ ID NO: 1:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3580 base pairs  
 (B) TYPE: nucleic acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

CCCGGGTGC	C	TCCCCTAAC	C	TACTTATAG	A	C	TATTTC	T	TGCTCTGCA	G	CATGGACCA	60
AAGAGAAATT	C	TGCAAGT	T	CCTGGATGA	G	GCCCCAAAGC	A	AAGAAAATT	C	TAAAGAGGA	120	
GTTTCCAAT	G	AATTCTGA	A	AGCTAAAAG	G	C	AATCTACC	A	AGTACAAGG	C	AGACAAAAC	180
CTATCCTACA	A	ACTGTGGCTG	A	GAAGCCAA	G	A	ATATCAAG	A	AAAACAGAT	A	TAAGGATAT	240
TTTGCCCTAT	G	GATTATAGCC	G	GGTAGAACT	A	T	CCCTGATA	A	CCCTGATG	G	AGGATTCCAG	300
CTACATCAAT	C	GCCAACCTCA	T	TAAGGGAGT	T	T	ATGGACCC	A	AGGCTTATA	T	TTGCCACCCA	360
GGGTCCCTTA	T	TCTACAAACCC	T	CTCTGGACTT	C	T	CTGGAGGATG	A	TTTGGGAAT	A	ATAGTGTCC	420
TATCATTGTT	A	ATGGCATGCA	T	TGGAGTATGA	A	A	ATGGGAAAG	A	AAAAGTGTG	G	AGCGCTACTG	480
GGCTGAGCCA	G	GGAGAGATGC	A	AGCTGGAATT	T	G	GCCCCTTTC	T	TCTGTATCCT	T	GTGAAGCTGA	540
AAAAAGGAAA	T	TCTGATTATA	T	AAATCAGGAC	T	C	TCTAAAAGTT	A	AGTTCAATA	G	GTGAAACTCG	600
AACTATCTAC	C	CAGTTCAATT	A	ACAAGAATTG	G	G	CCAGACCAT	G	ATGTACCTT	C	CATCTATAGA	660
CCCTATTCTT	G	GAGCTCATCT	G	GGGATGTACG	T	T	GGTTACCAA	G	GAGGTGACA	T	GTGTTCCCAT	720
ATGCATTAC	A	TGCAGTGCTG	G	GCTGTGGAAG	G	A	ACTGGTGT	T	ATTGTGCTA	T	TTGATTATAC	780
ATGGATGTTG	T	CTAAAAGATG	G	GGATAATTCC	T	G	TGAGAACTTC	A	GTGTTTCA	G	TTTGATCCG	840
GGAAATGCGG	A	ACACAGAGGC	C	CTTCATTAGT	T	C	AAACACGAG	G	AACTGGTCTA	A	900	
CAATGCTGTA	T	TTAGAACTAT	T	TTAAGAGACA	G	A	TGAGATGTT	A	ATCAGAGATA	A	ACATTCTGG	960
AACAGAGAGT	A	CAAGCAAAGC	A	ATTGTATTCC	T	G	AGGAAAAT	C	ACACTCTCC	A	AAGCAGACTC	1020
TTATTCTCCT	A	AATTACCAA	A	AAAGTACCA	A	A	AAAGCAGCA	A	AAATGATGA	A	ACCAACAAAG	1080
GACAAAAATG	G	GAAATCAAAG	A	AATCTTCTTC	C	T	TTTGACTTT	G	AAATAAGTGC	A	1140	
AAAAGAAGAG	C	CTAGTTTGC	A	ACCCCTGCTAA	T	A	GGACTTCTG	A	TTCTGGAGCT	T	1200	
AAATTACAGT	T	TTTGACAAAA	A	ATGCTGACAC	A	A	GGCAGACAA	G	AGGCATTCC	G	1260	
AATAGTTGG	G	GAGCCTCTTC	A	AGAAGCATCA	A	A	AGTTGGAT	T	TTGGCTCTC	T	TTTGTTGA	1320
GGGATGTTCT	A	AATTCTAAC	C	CTGAAATGC	G	A	CGAGGAAGA	T	TTTTAATT	C	AAAGGTGCC	1380
AATAACACGG	C	ACCAATCAA	C	TCCTTTGA	T	A	AGAGAGAAA	C	AAAGGAGGT	G	1440	

GGACAGCAAG GAAAACTTT CTTATTTGGA ATCTCAACCA CATGATTCTT GTTTGTAGA	1500
GATGCAGGCT CAAAAAGTAA TGCATGTTTC TTCAGCAGAA CTGAATTATT CACTGCCATA	1560
TGACTCTAAA CACCAAATAC GTAATGCCTC TAATGTAAG CACCATGACT CTAGTGCTCT	1620
TGGTGTATAT TCTTACATAC CTTAGTGGAA AAATCCTTAT TTTTCATCAT GGCTCCAAG	1680
TGGTACCAAGT TCTAAGATGT CTCTTGATTT ACCTGAGAAG CAAGATGGAA CTGTTTTCC	1740
TTCTTCTCTG TTGCCAACAT CCTCTACATC CCTCTTCTCT TATTACAATT CACATGATTC	1800
TTTATCACTG AATTCTCCAA CCAATATTTC CTCACTATTG AACCAGGAGT CAGCTGTACT	1860
AGCAACTGCT CCAAGGATAG ATGATGAAAT CCCCCCTCCA CTTCTGTAC GGACACCTGA	1920
ATCATTATTGT GTGGTTGAGG AAGCTGGAGA ATTCTCACCA AATGTTCCCA AATCCTTATC	1980
CTCAGCTGTG AAGGTAAAAA TTGGAACATC ACTGGAATGG GGTGGAACAT CTGAACCAAA	2040
GAAATTGTAT GACTCTGTGA TACTTAGACC AAGCAAGAGT GTAAAACCTCC GAAGTCCTAA	2100
ATCAGAACTA CATCAAGATC GTTCTTCTCC CCCACCTCCT CTCCCAGAAA GAACTCTAGA	2160
GTCCTCTTT CTTGCCGATG AAGATTGTAT GCAGGCCAA TCTATAGAAA CATATTCTAC	2220
TAGCTATCCT GACACCATGG AAAATTCAAC ATCTTCAAAA CAGACACTGA AGACTCCTGG	2280
AAAAAGTTTC ACAAGGAGTA AGAGTTGAA AATTTGCGA AACATGAAAA AGAGTATCTG	2340
TAATTCTTGC CCACAAACAA AGCCTGCAGA ATCTGTTCAAG TCAAATAACT CCAGCTCATT	2400
TCTGAATTTT GGTTTGCAA ACCGTTTTTC AAAACCCAAA GGACCAAGGA ATCCACCACC	2460
AACTTGGAAAT ATTTAATAAA ACTCCAGATT TATAATAATA TGCGCTGCAA GTACACCTGC	2520
AAATAAAACT ACTAGAATAC TGCTAGTTAA AATAAGTGCT CTATATGCAT AATATCAAAT	2580
ATGAAGATAT GCTAATGTGT TAATAGCTTT TAAAAGAAAA GCAAAATGCC AATAAGTGC	2640
AGTTTTGCAT TTTCATATCA TTTGCATTGA GTTGAAAAGT GCAAATAAAA GTTTGTCACT	2700
TGAGCTTATG TACAGAATGC TATATGAGAA ACACCTTTAG AATGGATTAA TTTTCATTT	2760
TTGCCAGTTA TTTTATTTT CTTTTACTTT TTTACATAAA CATAAACTTC AAAAGGTTG	2820
TAAGATTGG ATCTCAACTA ATTTCTACAT TGCCAGAATA TACTATAAAA AGTTAAAAAA	2880
AAACTTACTT TGTGGGTTGC AATACAAACT GCTCTTGACA ATGACTATTG CCTGACAGTT	2940
ATTTTGCCCT AAATGGAGTA TACCTTGAA ATCTTCCAA ATGTTGTGGA AAACCTGGAAT	3000
ATTAAGAAAA TGAGAAATT TATTATTAG AATAAAATGT GCAAATAATG ACAATTATTT	3060
GAATGTAACA AGGAATTCAA CTGAAATCCT GATAAGTTT AACCAAAGTC ATTAAATTAC	3120
CAATTCTAGA AAAGTAATCA ATGAAATATA ATAGCTATCT TTGTTGAGCA AAAGATATAA	3180
ATTGTATATG TTTATACAGG ATCTTTCAGA TCATGTGCAA TTTTATCTA ACCAATCAGA	3240
AATACTAGTT TAAAATGAAT TTCTATATGA ATATGGATCT GCCATAAGAA AATCTAGTTC	3300
AACTCTAATT TTATGTAGTA AATAAATTGG CAGGTAATTG TTTTACAAA GAATCCACCT	3360
GACTTCCCCT AATGCATTAA AAATATTTTT ATTTAAATAA CTTTATTTAT AACTTTAGA	3420
AACATGTAGT ATTGTTAAA CATCATTGT TCTTCAGTAT TTTTCATTTG GAAGTCCAAT	3480
AGGGCAAATT GAATGAAGTA TTATTATCTG TCTCTGTAG TACAATGTAT CCAACAGACA	3540
CTCAATAAAC TTTTGTTG TTAAAAAAA AAAAAAAA	3580

## (2) INFORMATION FOR SEQ ID NO: 2:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH:	807 amino acids
(B) TYPE:	amino acid
(C) STRANDEDNESS:	single
(D) TOPOLOGY:	linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Asp Gln Arg Glu Ile Leu Gln Lys Phe Leu Asp Glu Ala Gln Ser  
1 5 10 15

Lys Lys Ile Thr Lys Glu Glu Phe Ala Asn Glu Phe Leu Lys Leu Lys  
20 25 30

Arg Gln Ser Thr Lys Tyr Lys Ala Asp Lys Thr Tyr Pro Thr Thr Val  
35 40 45

Ala Glu Lys Pro Lys Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu  
50 55 60

Pro Tyr Asp Tyr Ser Arg Val Glu Leu Ser Leu Ile Thr Ser Asp Glu  
65 70 75 80

Asp Ser Ser Tyr Ile Asn Ala Asn Phe Ile Lys Gly Val Tyr Gly Pro  
85 90 95

Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp  
100 105 110

Phe Trp Arg Met Ile Trp Glu Tyr Ser Val Leu Ile Ile Val Met Ala  
115 120 125

Cys Met Glu Tyr Glu Met Gly Lys Lys Lys Cys Glu Arg Tyr Trp Ala  
130 135 140

Glu Pro Gly Glu Met Gln Leu Glu Phe Gly Pro Phe Ser Val Ser Cys  
145 150 155 160

Glu Ala Glu Lys Arg Lys Ser Asp Tyr Ile Ile Arg Thr Leu Lys Val  
165 170 175

Lys Phe Asn Ser Glu Thr Arg Thr Ile Tyr Gln Phe His Tyr Lys Asn  
180 185 190

Trp Pro Asp His Asp Val Pro Ser Ser Ile Asp Pro Ile Leu Glu Leu  
195 200 205

Ile Trp Asp Val Arg Cys Tyr Gln Glu Asp Asp Ser Val Pro Ile Cys  
210 215 220

Ile His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Ile  
225 230 235 240

Asp Tyr Thr Trp Met Leu Leu Lys Asp Gly Ile Ile Pro Glu Asn Phe

245                    250                    255  
Ser Val Phe Ser Leu Ile Arg Glu Met Arg Thr Gln Arg Pro Ser Leu  
260                    265                    270  
  
Val Gln Thr Gln Glu Gln Tyr Glu Leu Val Tyr Asn Ala Val Leu Glu  
275                    280                    285  
  
Leu Phe Lys Arg Gln Met Asp Val Ile Arg Asp Lys His Ser Gly Thr  
290                    295                    300  
  
  
Glu Ser Gln Ala Lys His Cys Ile Pro Glu Lys Asn His Thr Leu Gln  
305                    310                    315                    320  
  
Ala Asp Ser Tyr Ser Pro Asn Leu Pro Lys Ser Thr Thr Lys Ala Ala  
325                    330                    335  
  
Lys Met Met Asn Gln Gln Arg Thr Lys Met Glu Ile Lys Glu Ser Ser  
340                    345                    350  
  
Ser Phe Asp Phe Arg Thr Ser Glu Ile Ser Ala Lys Glu Glu Leu Val  
355                    360                    365  
  
Leu His Pro Ala Lys Ser Ser Thr Ser Phe Asp Phe Leu Glu Leu Asn  
370                    375                    380  
  
Tyr Ser Phe Asp Lys Asn Ala Asp Thr Thr Met Lys Trp Gln Thr Lys  
385                    390                    395                    400  
  
Ala Phe Pro Ile Val Gly Glu Pro Leu Gln Lys His Gln Ser Leu Asp  
405                    410                    415  
  
Leu Gly Ser Leu Leu Phe Glu Gly Cys Ser Asn Ser Lys Pro Val Asn  
420                    425                    430  
  
Ala Ala Gly Arg Tyr Phe Asn Ser Lys Val Pro Ile Thr Arg Thr Lys  
435                    440                    445  
  
Ser Thr Pro Phe Glu Leu Ile Gln Gln Arg Glu Thr Lys Glu Val Asp  
450                    455                    460  
  
Ser Lys Glu Asn Phe Ser Tyr Leu Glu Ser Gln Pro His Asp Ser Cys  
465                    470                    475                    480  
  
Phe Val Glu Met Gln Ala Gln Lys Val Met His Val Ser Ser Ala Glu  
485                    490                    495  
  
Leu Asn Tyr Ser Leu Pro Tyr Asp Ser Lys His Gln Ile Arg Asn Ala

500

505

510

Ser Asn Val Lys His His Asp Ser Ser Ala Leu Gly Val Tyr Ser Tyr  
515 520 525

Ile Pro Leu Val Glu Asn Pro Tyr Phe Ser Ser Trp Pro Pro Ser Gly  
530 535 540

Thr Ser Ser Lys Met Ser Leu Asp Leu Pro Glu Lys Gln Asp Gly Thr  
545 550 555 560

Val Phe Pro Ser Ser Leu Leu Pro Thr Ser Ser Thr Ser Leu Phe Ser  
565 570 575

Tyr Tyr Asn Ser His Asp Ser Leu Ser Leu Asn Ser Pro Thr Asn Ile  
580 585 590

Ser Ser Leu Leu Asn Gln Glu Ser Ala Val Leu Ala Thr Ala Pro Arg  
595 600 605

Ile Asp Asp Glu Ile Pro Pro Pro Leu Pro Val Arg Thr Pro Glu Ser  
610 615 620

Phe Ile Val Val Glu Glu Ala Gly Glu Phe Ser Pro Asn Val Pro Lys  
625 630 635 640

Ser Leu Ser Ser Ala Val Lys Val Lys Ile Gly Thr Ser Leu Glu Trp  
645 650 655

Gly Gly Thr Ser Glu Pro Lys Lys Phe Asp Asp Ser Val Ile Leu Arg  
660 665 670

Pro Ser Lys Ser Val Lys Leu Arg Ser Pro Lys Ser Glu Leu His Gln  
675 680 685

Asp Arg Ser Ser Pro Pro Pro Leu Pro Glu Arg Thr Leu Glu Ser  
690 695 700

Phe Phe Leu Ala Asp Glu Asp Cys Met Gln Ala Gln Ser Ile Glu Thr  
705 710 715 720

Tyr Ser Thr Ser Tyr Pro Asp Thr Met Glu Asn Ser Thr Ser Ser Lys  
725 730 735

Gln Thr Leu Lys Thr Pro Gly Lys Ser Phe Thr Arg Ser Lys Ser Leu  
740 745 750

Lys Ile Leu Arg Asn Met Lys Lys Ser Ile Cys Asn Ser Cys Pro Pro  
755 760 765

Asn Lys Pro Ala Glu Ser Val Gln Ser Asn Asn Ser Ser Ser Phe Leu  
770 775 780

Asn Phe Gly Phe Ala Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn  
785 790 795 800

Pro Pro Pro Thr Trp Asn Ile  
805

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: The letter "Y" stands for C or T.  
The letter "V" stands for A, C or G.  
The letter "R" stands for A or G.  
The letter "N" stands for A, C, G or T.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GAYTTYTGGV RNATGRTNTG GGA

23

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: The letter "S" stands for C or G.  
The letter "Y" stands for C or T.  
The letter "N" stands for A, C, G  
or T.  
The letter "W" stands for A or T.  
The letter "R" stands for A or G.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

CGGCCSAYNC CNGCNSWRCA RTG

23

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 4 and 6 stand  
for an unspecified amino acid.  
"Xaa" in position 8 stands for  
either Glu or Asp.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Asp Phe Trp Xaa Met Xaa Trp Xaa  
1 5

(2) INFORMATION FOR SEQ ID NO: 6:

SSSD/90776. v01

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 7 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

(D) OTHER INFORMATION: "Xaa" in positions 3 and 6 stand for an unspecified amino acid.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

His Cys Xaa Ala Gly Xaa Gly  
1 5

## (2) INFORMATION FOR SEQ ID NO: 7:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CACCGTTCGA GTATTCAGA TTGTGAAGAA GTCC

34

## (2) INFORMATION FOR SEQ ID NO: 8:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

SSSD/90776. v01

GGACTTCTTC ACAATCTGAA ATACTCGAAC GGTG

34

## (2) INFORMATION FOR SEQ ID NO: 9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

CCGTTATGTG AGGAAGAGCC ACATTACAGG ACC

33

## (2) INFORMATION FOR SEQ ID NO: 10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGTCCTGTAA TGTGGCTCTT CCTCACATAA CGG

33

## (2) INFORMATION FOR SEQ ID NO: 11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGCATGCATG GACTATGAAA TGG

23

## (2) INFORMATION FOR SEQ ID NO: 12:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CGTACATCCC AGATGAGCTC AAGAATAGGG

30

## (2) INFORMATION FOR SEQ ID NO: 13:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser  
1 5 10

## (2) INFORMATION FOR SEQ ID NO: 14:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

His Cys Ser Ala Gly  
1 5

## (2) INFORMATION FOR SEQ ID NO: 15:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Ser Trp Pro Pro Ser Gly Thr Ser Ser Lys Met Ser Leu Asp Asp Leu  
1 5 10 15

Pro Glu Lys Gln Asp Gly Thr Val Phe Pro Ser Ser Leu Leu Pro  
20 25 30

## (2) INFORMATION FOR SEQ ID NO: 16:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Tyr Ser Leu Pro Tyr Asp Ser Lys His Gln Ile Arg Asn Ala Ser Asn  
1 5 10 15

Val Lys His His Asp Ser Ser Ala Leu Gly Val Tyr Ser Tyr  
20 25 30

## (2) INFORMATION FOR SEQ ID NO: 17:

## (i) SEQUENCE CHARACTERISTICS:

SSSD/90776. v01

(A) LENGTH: 30 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

His Thr Leu Gln Ala Asp Ser Tyr Ser Pro Asn Leu Pro Lys Ser Thr  
1 5 10 15

Thr Lys Ala Ala Lys Met Met Asn Gln Gln Arg Thr Lys Cys  
20 25 30

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 802 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Met Asp Gln Arg Glu Ile Leu Gln Gln Leu Leu Lys Glu Ala Gln Lys  
1 5 10 15

Lys Lys Leu Asn Ser Glu Glu Phe Ala Ser Glu Phe Leu Lys Leu Lys  
20 25 30

Arg Gln Ser Thr Lys Tyr Lys Ala Asp Lys Ile Tyr Pro Thr Thr Val  
35 40 45

Ala Gln Arg Pro Lys Asn Ile Lys Lys Asn Arg Tyr Lys Asp Ile Leu  
50 55 60

Pro Tyr Asp His Ser Leu Val Glu Leu Ser Leu Leu Thr Ser Asp Glu  
65 70 75 80

Asp Ser Ser Tyr Ile Asn Ala Ser Phe Ile Lys Gly Val Tyr Gly Pro  
85 90 95

Lys Ala Tyr Ile Ala Thr Gln Gly Pro Leu Ser Thr Thr Leu Leu Asp  
100 105 110

Phe Trp Arg Met Ile Trp Glu Tyr Arg Ile Leu Val Ile Val Met Ala  
115 120 125

Cys Met Glu Phe Glu Met Gly Lys Lys Cys Glu Arg Tyr Trp Ala  
130 135 140

Glu Pro Gly Glu Thr Gln Leu Gln Phe Gly Pro Phe Ser Ile Ser Cys  
145 150 155 160

Glu Ala Glu Lys Lys Ser Asp Tyr Lys Ile Arg Thr Leu Lys Ala  
165 170 175

Lys Phe Asn Asn Glu Thr Arg Ile Ile Tyr Gln Phe His Tyr Lys Asn  
180 185 190

Trp Pro Asp His Asp Val Pro Ser Ser Ile Asp Pro Ile Leu Gln Leu  
195 200 205

Ile Trp Asp Met Arg Cys Tyr Gln Glu Asp Asp Cys Val Pro Ile Cys  
210 215 220

Ile His Cys Ser Ala Gly Cys Gly Arg Thr Gly Val Ile Cys Ala Val  
225 230 235 240

Asp Tyr Thr Trp Met Leu Leu Lys Asp Gly Ile Ile Pro Lys Asn Phe  
245 250 255

Ser Val Phe Asn Leu Ile Gln Glu Met Arg Thr Gln Arg Pro Ser Leu  
260 265 270

Val Gln Thr Gln Glu Gln Tyr Glu Leu Val Tyr Ser Ala Val Leu Glu  
275 280 285

Leu Phe Lys Arg His Met Asp Val Ile Ser Asp Asn His Leu Gly Arg  
290 295 300

Glu Ile Gln Ala Gln Cys Ser Ile Pro Glu Gln Ser Leu Thr Val Glu  
305 310 315 320

Ala Asp Ser Cys Pro Leu Asp Leu Pro Lys Asn Ala Met Arg Asp Val  
325 330 335

Lys Thr Thr Asn Gln His Ser Lys Gln Gly Ala Glu Ala Glu Ser Thr  
340 345 350

Gly Gly Ser Ser Leu Gly Leu Arg Thr Ser Thr Met Asn Ala Glu Glu  
355 360 365

Glu Leu Val Leu His Ser Ala Lys Ser Ser Pro Ser Phe Asn Cys Leu  
370 375 380

Glu Leu Asn Cys Gly Cys Asn Asn Lys Ala Val Ile Thr Arg Asn Gly  
385 390 395 400

Gln Ala Arg Ala Ser Pro Val Val Gly Glu Pro Leu Gln Lys Tyr Gln  
405 410 415

Ser Leu Asp Phe Gly Ser Met Leu Phe Gly Ser Cys Pro Ser Ala Leu  
420 425 430

Pro Ile Asn Thr Ala Asp Arg Tyr His Asn Ser Lys Gly Pro Val Lys  
435 440 445

Arg Thr Lys Ser Thr Pro Phe Glu Leu Ile Gln Gln Arg Lys Thr Asn  
450 455 460

Asp Leu Ala Val Gly Asp Gly Phe Ser Cys Leu Glu Ser Gln Leu His  
465 470 475 480

Glu His Tyr Ser Leu Arg Glu Leu Gln Val Gln Arg Val Ala His Val  
485 490 495

Ser Ser Glu Glu Leu Asn Tyr Ser Leu Pro Gly Ala Cys Asp Ala Ser  
500 505 510

Cys Val Pro Arg His Ser Pro Gly Ala Leu Arg Val His Leu Tyr Thr  
515 520 525

Ser Leu Ala Glu Asp Pro Tyr Phe Ser Ser Ser Pro Pro Asn Ser Ala  
530 535 540

Asp Ser Lys Met Ser Phe Asp Leu Pro Glu Lys Gln Asp Gly Ala Thr  
545 550 555 560

Ser Pro Gly Ala Leu Leu Pro Ala Ser Ser Thr Thr Ser Phe Phe Tyr  
565 570 575

Ser Asn Pro His Asp Ser Leu Val Met Asn Thr Leu Thr Ser Phe Ser  
580 585 590

Pro Pro Leu Asn Gln Glu Thr Ala Val Glu Ala Pro Ser Arg Arg Thr  
595 600 605

Asp Asp Glu Ile Pro Pro Pro Leu Pro Glu Arg Thr Pro Glu Ser Phe  
610 615 620

Ile Val Val Glu Glu Ala Gly Glu Pro Ser Pro Arg Val Thr Glu Ser  
625 630 635 640

Leu Pro Leu Val Val Thr Phe Gly Ala Ser Pro Glu Cys Ser Gly Thr  
645 650 655

Ser Glu Met Lys Ser His Asp Ser Val Gly Phe Thr Pro Ser Lys Asn  
660 665 670

Val Lys Leu Arg Ser Pro Lys Ser Asp Arg His Gln Asp Gly Ser Pro  
675 680 685

Pro Pro Pro Leu Pro Glu Arg Thr Leu Glu Ser Phe Phe Leu Ala Asp  
690 695 700

Glu Asp Cys Ile Gln Ala Gln Ala Val Gln Thr Ser Ser Thr Ser Tyr  
705 710 715 720

Pro Glu Thr Thr Glu Asn Ser Thr Ser Ser Lys Gln Thr Leu Arg Thr  
725 730 735

Pro Gly Lys Ser Phe Thr Arg Ser Lys Ser Leu Lys Ile Phe Arg Asn  
740 745 750

Met Lys Lys Ser Val Cys Asn Ser Ser Ser Pro Ser Lys Pro Thr Glu  
755 760 765

Arg Val Gln Pro Lys Asn Ser Ser Ser Phe Leu Asn Phe Gly Phe Gly  
770 775 780

Asn Arg Phe Ser Lys Pro Lys Gly Pro Arg Asn Pro Pro Ser Ala Trp  
785 790 795 800

Asn Met